

SEQUENCE LISTING



<110> Prof. Dr. Werner Seeger

<120> Novel chimeric plasminogen activators and their pharmaceutical use

<130> 607927-000001

<140> US/10/583,785

<141> 2006-06-19

<160> 26

<210> 1

<211> 1143

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (1143)

<223> Coding sequence of the surfactant protein B precursor

<400> 1

atg gct gag tca cac ctg ctg cag tgg ctg ctg ctg ctg ctg ccc acg	48
Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr	
1 5 10 15	
ctc tgt ggc cca ggc act gct gcc tgg acc acc tca tcc ttg gcc tgt	96
Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys	
20 25 30	
gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag caa gca ttg cag	144
Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln	
35 40 45	
tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga	192
Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly	
50 55 60	
gcc gat gac cta tgc caa gag tgt gag gac atc gtc cac atc ctt aac	240
Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn	
65 70 75 80	
aag atg gcc aag gag gcc att ttc cag gac acg atg agg aag ttc ctg	288
Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu	
85 90 95	
gag cag gag tgc aac gtc ctc ccc ttg aag ctg ctc atg ccc cag tgc	336
Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys	
100 105 110	
aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag	384
Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln	
115 120 125	
aac cag act gac tca aac ggc atc tgt atg cac ctg ggc ctg tgc aaa	432

Asn	Gln	Thr	Asp	Ser	Asn	Gly	Ile	Cys	Met	His	Leu	Gly	Leu	Cys	Lys	
130						135					140					
tcc	cgg	cag	cca	gag	cca	gag	cag	gag	cca	ggg	atg	tca	gac	ccc	ctg	480
Ser	Arg	Gln	Pro	Glu	Pro	Glu	Gln	Glu	Pro	Gly	Met	Ser	Asp	Pro	Leu	
145					150					155					160	
ccc	aaa	cct	ctg	cgg	gac	cct	ctg	cca	gac	cct	ctg	ctg	gac	aag	ctc	528
Pro	Lys	Pro	Leu	Arg	Asp	Pro	Leu	Pro	Asp	Pro	Leu	Leu	Asp	Lys	Leu	
				165					170					175		
gtc	ctc	cct	gtg	ctg	ccc	ggg	gcc	ctc	cag	gcg	agg	cct	ggg	cct	cac	576
Val	Leu	Pro	Val	Leu	Pro	Gly	Ala	Leu	Gln	Ala	Arg	Pro	Gly	Pro	His	
			180					185					190			
aca	cag	gat	ctc	tcc	gag	cag	caa	ttc	ccc	att	cct	ctc	ccc	tat	tgc	624
Thr	Gln	Asp	Leu	Ser	Glu	Gln	Gln	Phe	Pro	Ile	Pro	Leu	Pro	Tyr	Cys	
		195					200					205				
tgg	ctc	tgc	agg	gct	ctg	atc	aag	cgg	atc	caa	gcc	atg	att	ccc	aag	672
Trp	Leu	Cys	Arg	Ala	Leu	Ile	Lys	Arg	Ile	Gln	Ala	Met	Ile	Pro	Lys	
	210					215					220					
ggt	gcg	cta	gct	gtg	gca	gtg	gcc	cag	gtg	tgc	cgc	gtg	gta	cct	ctg	720
Gly	Ala	Leu	Ala	Val	Ala	Val	Ala	Gln	Val	Cys	Arg	Val	Val	Pro	Leu	
225					230					235					240	
gtg	gcg	ggc	ggc	atc	tgc	cag	tgc	ctg	gct	gag	cgc	tac	tcc	gtc	atc	768
Val	Ala	Gly	Gly	Ile	Cys	Gln	Cys	Leu	Ala	Glu	Arg	Tyr	Ser	Val	Ile	
				245					250					255		
ctg	ctc	gac	acg	ctg	ctg	ggc	cgc	atg	ctg	ccc	cag	ctg	gtc	tgc	cgc	816
Leu	Leu	Asp	Thr	Leu	Leu	Gly	Arg	Met	Leu	Pro	Gln	Leu	Val	Cys	Arg	
			260					265					270			
ctc	gtc	ctc	cgg	tgc	tcc	atg	gat	gac	agc	gct	ggc	cca	agg	tcg	ccg	864
Leu	Val	Leu	Arg	Cys	Ser	Met	Asp	Asp	Ser	Ala	Gly	Pro	Arg	Ser	Pro	
		275					280					285				
aca	gga	gaa	tgg	ctg	ccg	cga	gac	tct	gag	tgc	cac	ctc	tgc	atg	tcc	912
Thr	Gly	Glu	Trp	Leu	Pro	Arg	Asp	Ser	Glu	Cys	His	Leu	Cys	Met	Ser	
	290					295					300					
gtg	acc	acc	cag	gcc	ggg	aac	agc	agc	gag	cag	gcc	ata	cca	cag	gca	960
Val	Thr	Thr	Gln	Ala	Gly	Asn	Ser	Ser	Glu	Gln	Ala	Ile	Pro	Gln	Ala	
305					310					315					320	
atg	ctc	cag	gcc	tgt	gtt	ggc	tcc	tgg	ctg	gac	agg	gaa	aag	tgc	aag	1008
Met	Leu	Gln	Ala	Cys	Val	Gly	Ser	Trp	Leu	Asp	Arg	Glu	Lys	Cys	Lys	
				325					330					335		
caa	ttt	gtg	gag	cag	cac	acg	ccc	cag	ctg	ctg	acc	ctg	gtg	ccc	agg	1056
Gln	Phe	Val	Glu	Gln	His	Thr	Pro	Gln	Leu	Leu	Thr	Leu	Val	Pro	Arg	
			340					345					350			
ggc	tgg	gat	gcc	cac	acc	acc	tgc	cag	gcc	ctc	ggg	gtg	tgt	ggg	acc	1104
Gly	Trp	Asp	Ala	His	Thr	Thr	Cys	Gln	Ala	Leu	Gly	Val	Cys	Gly	Thr	

355		360		365	
atg tcc agc cct ctc cag tgt atc cac agc ccc gac ctt					1143
Met Ser Ser Pro Leu Gln Cys Ile His Ser Pro Asp Leu					
370		375		380	

<210> 2  
 <211> 837  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1) ... (837)  
 <223> Coding sequence of SP-B precursor lacking the C-terminal propeptide

<400> 2

atg gct gag tca cac ctg ctg cag tgg ctg ctg ctg ctg ctg ccc acg	48
Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr	
1 5 10 15	
ctc tgt ggc cca ggc act gct gcc tgg acc acc tca tcc ttg gcc tgt	96
Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys	
20 25 30	
gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag caa gca ttg cag	144
Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln	
35 40 45	
tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga	192
Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly	
50 55 60	
gcc gat gac cta tgc caa gag tgt gag gac atc gtc cac atc ctt aac	240
Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn	
65 70 75 80	
aag atg gcc aag gag gcc att ttc cag gac acg atg agg aag ttc ctg	288
Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu	
85 90 95	
gag cag gag tgc aac gtc ctc ccc ttg aag ctg ctc atg ccc cag tgc	336
Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys	
100 105 110	
aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag	384
Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln	
115 120 125	
aac cag act gac tca aac ggc atc tgt atg cac ctg ggc ctg tgc aaa	432
Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys	
130 135 140	
tcc cgg cag cca gag cca gag cag gag cca ggg atg tca gac ccc ctg	480
Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu	

145		150		155		160	
ccc aaa cct ctg cgg gac cct ctg cca gac cct ctg ctg gac aag ctc							528
Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu							
		165		170		175	
gtc ctc cct gtg ctg ccc ggg gcc ctc cag gcg agg cct ggg cct cac							576
Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His							
		180		185		190	
aca cag gat ctc tcc gag cag caa ttc ccc att cct ctc ccc tat tgc							624
Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys							
		195		200		205	
tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att ccc aag							672
Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys							
		210		215		220	
ggt gcg cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta cct ctg							720
Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu							
		225		230		235	240
gtg gcg ggc ggc atc tgc cag tgc ctg gct gag cgc tac tcc gtc atc							768
Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile							
		245		250		255	
ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc tgc cgc							816
Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg							
		260		265		270	
ctc gtc ctc cgg tgc tcc atg							837
Leu Val Leu Arg Cys Ser Met							
		275					

<210> 3

<211> 237

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (237)

<223> Coding sequence of the mature surfactant protein B

<400> 3

ttc ccc att cct ctc ccc tat tgc tgg ctc tgc agg gct ctg atc aag																	48
Phe Pro Ile Pro Leu Pro Tyr Cys Trp Leu Cys Arg Ala Leu Ile Lys																	
1				5				10								15	
cgg atc caa gcc atg att ccc aag ggt gcg cta gct gtg gca gtg gcc																	96
Arg Ile Gln Ala Met Ile Pro Lys Gly Ala Leu Ala Val Ala Val Ala																	
			20				25						30				
cag gtg tgc cgc gtg gta cct ctg gtg gcg ggc ggc atc tgc cag tgc																	144
Gln Val Cys Arg Val Val Pro Leu Val Ala Gly Gly Ile Cys Gln Cys																	

35	40	45	
ctg gct gag cgc tac tcc gtc atc ctg ctc gac acg ctg ctg ggc cgc			192
Leu Ala Glu Arg Tyr Ser Val Ile Leu Leu Asp Thr Leu Leu Gly Arg			
50	55	60	
atg ctg ccc cag ctg gtc tgc cgc ctc gtc ctc cgg tgc tcc atg			237
Met Leu Pro Gln Leu Val Cys Arg Leu Val Leu Arg Cys Ser Met			
65	70	75	
<210> 4			
<211> 1293			
<212> DNA			
<213> Homo sapiens			
<220>			
<221> CDS			
<222> (1) ... (1293)			
<223> Coding sequence of the single-chain urokinase-plasminogen activator			
<400> 4			
atg aga gcc ctg ctg gcg cgc ctg ctt ctc tgc gtc ctg gtc gtg agc			48
Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser			
1	5	10	15
gac tcc aaa ggc agc aat gaa ctt cat caa gtt cca tcg aac tgt gac			96
Asp Ser Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp			
20	25	30	
tgt cta aat gga gga aca tgt gtg tcc aac aag tac ttc tcc aac att			144
Cys Leu Asn Gly Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile			
35	40	45	
cac tgg tgc aac tgc cca aag aaa ttc gga ggg cag cac tgt gaa ata			192
His Trp Cys Asn Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile			
50	55	60	
gat aag tca aaa acc tgc tat gag ggg aat ggt cac ttt tac cga gga			240
Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly			
65	70	75	80
aag gcc agc act gac acc atg ggc cgg ccc tgc ctg ccc tgg aac tct			288
Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser			
85	90	95	
gcc act gtc ctt cag caa acg tac cat gcc cac aga tct gat gct ctt			336
Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu			
100	105	110	
cag ctg ggc ctg ggg aaa cat aat tac tgc agg aac cca gac aac cgg			384
Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg			
115	120	125	
agg cga ccc tgg tgc tat gtg cag gtg ggc cta aag ccg ctt gtc caa			432
Arg Arg Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln			

130		135		140	
gag tgc atg gtg cat gac tgc gca gat gga aaa aag ccc tcc tct cct					480
Glu Cys Met Val His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro					
145		150		155	160
cca gaa gaa tta aaa ttt cag tgt ggc caa aag act ctg agg ccc cgc					528
Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg					
	165		170		175
ttt aag att att ggg gga gaa ttc acc acc atc gag aac cag ccc tgg					576
Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp					
	180		185		190
ttt gcg gcc atc tac agg agg cac cgg ggg ggc tct gtc acc tac gtg					624
Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val					
	195		200		205
tgt gga ggc agc ctc atc agc cct tgc tgg gtg atc agc gcc aca cac					672
Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His					
	210		215		220
tgc ttc att gat tac cca aag aag gag gac tac atc gtc tac ctg ggt					720
Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly					
	225		230		240
cgc tca agg ctt aac tcc aac acg caa ggg gag atg aag ttt gag gtg					768
Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val					
	245		250		255
gaa aac ctc atc cta cac aag gac tac agc gct gac acg ctt gct cac					816
Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His					
	260		265		270
cac aac gac att gcc ttg ctg aag atc cgt tcc aag gag ggc agg tgt					864
His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys					
	275		280		285
gcg cag cca tcc cgg act ata cag acc atc tgc ctg ccc tcg atg tat					912
Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr					
	290		295		300
aac gat ccc cag ttt ggc aca agc tgt gag atc act ggc ttt gga aaa					960
Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys					
	305		310		320
gag aat tct acc gac tat ctc tat ccg gag cag ctg aaa atg act gtt					1008
Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val					
	325		330		335
gtg aag ctg att tcc cac cgg gag tgt cag cag ccc cac tac tac ggc					1056
Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly					
	340		345		350
tct gaa gtc acc acc aaa atg ctg tgt gct gct gac cca cag tgg aaa					1104
Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys					

355	360	365	
aca gat tcc tgc cag gga gac tca ggg gga ccc ctc gtc tgt tcc ctc			1152
Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu			
370	375	380	
caa ggc cgc atg act ttg act gga att gtg agc tgg ggc cgt gga tgt			1200
Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys			
385	390	395	400
gcc ctg aag gac aag cca ggc gtc tac acg aga gtc tca cac ttc tta			1248
Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu			
	405	410	415
ccc tgg atc cgc agt cac acc aag gaa gag aat ggc ctg gcc ctc			1293
Pro Trp Ile Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu			
	420	425	430

<210> 5

<211> 828

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (828)

<223> Coding sequence of low mw two-chain urokinase-plasminogen activator

<400> 5

aag ccc tcc tct cct cca gaa gaa tta aaa ttt cag tgt ggc caa aag	48
Lys Pro Ser Ser Pro Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys	
1	5
act ctg agg ccc cgc ttt aag att att ggg gga gaa ttc acc acc atc	96
Thr Leu Arg Pro Arg Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile	
	20
gag aac cag ccc tgg ttt gcg gcc atc tac agg agg cac cgg ggg ggc	144
Glu Asn Gln Pro Trp Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly	
	35
tct gtc acc tac gtg tgt gga ggc agc ctc atc agc cct tgc tgg gtg	192
Ser Val Thr Tyr Val Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val	
	50
atc agc gcc aca cac tgc ttc att gat tac cca aag aag gag gac tac	240
Ile Ser Ala Thr His Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr	
	65
atc gtc tac ctg ggt cgc tca agg ctt aac tcc aac acg caa ggg gag	288
Ile Val Tyr Leu Gly Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu	
	85
atg aag ttt gag gtg gaa aac ctc atc cta cac aag gac tac agc gct	336



Met	Lys	Phe	Glu	Val	Glu	Asn	Leu	Ile	Leu	His	Lys	Asp	Tyr	Ser	Ala		
			100					105					110				
gac	acg	ctt	gct	cac	cac	aac	gac	att	gcc	ttg	ctg	aag	atc	cgt	tcc		384
Asp	Thr	Leu	Ala	His	His	Asn	Asp	Ile	Ala	Leu	Leu	Lys	Ile	Arg	Ser		
		115					120					125					
aag	gag	ggc	agg	tgt	gcg	cag	cca	tcc	cgg	act	ata	cag	acc	atc	tgc		432
Lys	Glu	Gly	Arg	Cys	Ala	Gln	Pro	Ser	Arg	Thr	Ile	Gln	Thr	Ile	Cys		
	130					135					140						
ctg	ccc	tcg	atg	tat	aac	gat	ccc	cag	ttt	ggc	aca	agc	tgt	gag	atc		480
Leu	Pro	Ser	Met	Tyr	Asn	Asp	Pro	Gln	Phe	Gly	Thr	Ser	Cys	Glu	Ile		
145					150				155					160			
act	ggc	ttt	gga	aaa	gag	aat	tct	acc	gac	tat	ctc	tat	ccg	gag	cag		528
Thr	Gly	Phe	Gly	Lys	Glu	Asn	Ser	Thr	Asp	Tyr	Leu	Tyr	Pro	Glu	Gln		
				165				170						175			
ctg	aaa	atg	act	gtt	gtg	aag	ctg	att	tcc	cac	cgg	gag	tgt	cag	cag		576
Leu	Lys	Met	Thr	Val	Val	Lys	Leu	Ile	Ser	His	Arg	Glu	Cys	Gln	Gln		
			180					185					190				
ccc	cac	tac	tac	ggc	tct	gaa	gtc	acc	acc	aaa	atg	ctg	tgt	gct	gct		624
Pro	His	Tyr	Tyr	Gly	Ser	Glu	Val	Thr	Thr	Lys	Met	Leu	Cys	Ala	Ala		
		195					200					205					
gac	cca	cag	tgg	aaa	aca	gat	tcc	tgc	cag	gga	gac	tca	ggg	gga	ccc		672
Asp	Pro	Gln	Trp	Lys	Thr	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro		
	210					215					220						
ctc	gtc	tgt	tcc	ctc	caa	ggc	cgc	atg	act	ttg	act	gga	att	gtg	agc		720
Leu	Val	Cys	Ser	Leu	Gln	Gly	Arg	Met	Thr	Leu	Thr	Gly	Ile	Val	Ser		
225					230					235				240			
tgg	ggc	cgt	gga	tgt	gcc	ctg	aag	gac	aag	cca	ggc	gtc	tac	acg	aga		768
Trp	Gly	Arg	Gly	Cys	Ala	Leu	Lys	Asp	Lys	Pro	Gly	Val	Tyr	Thr	Arg		
				245				250					255				
gtc	tca	cac	ttc	tta	ccc	tgg	atc	cgc	agt	cac	acc	aag	gaa	gag	aat		816
Val	Ser	His	Phe	Leu	Pro	Trp	Ile	Arg	Ser	His	Thr	Lys	Glu	Gln	Asn		
			260				265						270				
ggc	ctg	gcc	ctc														828
Gly	Leu	Ala	Leu														
		275															

<210> 6

<211> 1671

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1) ... (837)

<223> Coding sequence of human SP-B precursor lacking the C-terminal



propeptide

<220>

<221> CDS

<222> (838) ... (843)

<223> Linker sequence

<220>

<221> CDS

<222> (844) ... (1671)

<223> Coding sequence of low mw two-chain urokinase-plasminogen activator

<400> 6

atg gct gag tca cac ctg ctg cag tgg ctg ctg ctg ctg ctg ccc acg	48
Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr	
1 5 10 15	
ctc tgt ggc cca ggc act gct gcc tgg acc acc tca tcc ttg gcc tgt	96
Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys	
20 25 30	
gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag caa gca ttg cag	144
Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln	
35 40 45	
tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga	192
Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly	
50 55 60	
gcc gat gac cta tgc caa gag tgt gag gac atc gtc cac atc ctt aac	240
Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn	
65 70 75 80	
aag atg gcc aag gag gcc att ttc cag gac acg atg agg aag ttc ctg	288
Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu	
85 90 95	
gag cag gag tgc aac gtc ctc ccc ttg aag ctg ctc atg ccc cag tgc	336
Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys	
100 105 110	
aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag	384
Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln	
115 120 125	
aac cag act gac tca aac ggc atc tgt atg cac ctg ggc ctg tgc aaa	432
Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys	
130 135 140	
tcc cgg cag cca gag cca gag cag gag cca ggg atg tca gac ccc ctg	480
Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu	
145 150 155 160	
ccc aaa cct ctg cgg gac cct ctg cca gac cct ctg ctg gac aag ctc	528
Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu	

165						170						175						
gtc	ctc	cct	gtg	ctg	ccc	ggg	gcc	ctc	cag	gcg	agg	cct	ggg	cct	cac			576
Val	Leu	Pro	Val	Leu	Pro	Gly	Ala	Leu	Gln	Ala	Arg	Pro	Gly	Pro	His			
			180					185					190					
aca	cag	gat	ctc	tcc	gag	cag	caa	ttc	ccc	att	cct	ctc	ccc	tat	tgc			624
Thr	Gln	Asp	Leu	Ser	Glu	Gln	Gln	Phe	Pro	Ile	Pro	Leu	Pro	Tyr	Cys			
		195					200					205						
tgg	ctc	tgc	agg	gct	ctg	atc	aag	cgg	atc	caa	gcc	atg	att	ccc	aag			672
Trp	Leu	Cys	Arg	Ala	Leu	Ile	Lys	Arg	Ile	Gln	Ala	Met	Ile	Pro	Lys			
	210					215					220							
ggc	gcg	cta	gct	gtg	gca	gtg	gcc	cag	gtg	tgc	cgc	gtg	gta	cct	ctg			720
Gly	Ala	Leu	Ala	Val	Ala	Val	Ala	Gln	Val	Cys	Arg	Val	Val	Pro	Leu			
225					230					235					240			
gtg	gcg	ggc	ggc	atc	tgc	cag	tgc	ctg	gct	gag	cgc	tac	tcc	gtc	atc			768
Val	Ala	Gly	Gly	Ile	Cys	Gln	Cys	Leu	Ala	Glu	Arg	Tyr	Ser	Val	Ile			
				245					250					255				
ctg	ctc	gac	acg	ctg	ctg	ggc	cgc	atg	ctg	ccc	cag	ctg	gtc	tgc	cgc			816
Leu	Leu	Asp	Thr	Leu	Leu	Gly	Arg	Met	Leu	Pro	Gln	Leu	Val	Cys	Arg			
			260					265					270					
ctc	gtc	ctc	cgg	tgc	tcc	atg	aag	ctt	aag	ccc	tcc	tct	cct	cca	gaa			864
Leu	Val	Leu	Arg	Cys	Ser	Met	Lys	Leu	Lys	Pro	Ser	Ser	Pro	Pro	Glu			
		275					280					285						
gaa	tta	aaa	ttt	cag	tgt	ggc	caa	aag	act	ctg	agg	ccc	cgc	ttt	aag			912
Glu	Leu	Lys	Phe	Gln	Cys	Gly	Gln	Lys	Thr	Leu	Arg	Pro	Arg	Phe	Lys			
	290					295					300							
att	att	ggg	gga	gaa	ttc	acc	acc	atc	gag	aac	cag	ccc	tgg	ttt	gcg			960
Ile	Ile	Gly	Gly	Glu	Phe	Thr	Thr	Ile	Glu	Asn	Gln	Pro	Trp	Phe	Ala			
305					310					315					320			
gcc	atc	tac	agg	agg	cac	cgg	ggg	ggc	tct	gtc	acc	tac	gtg	tgt	gga			1008
Ala	Ile	Tyr	Arg	Arg	His	Arg	Gly	Gly	Ser	Val	Thr	Tyr	Val	Cys	Gly			
				325					330					335				
ggc	agc	ctc	atc	agc	cct	tgc	tgg	gtg	atc	agc	gcc	aca	cac	tgc	ttc			1056
Gly	Ser	Leu	Ile	Ser	Pro	Cys	Trp	Val	Ile	Ser	Ala	Thr	His	Cys	Phe			
			340					345					350					
att	gat	tac	cca	aag	aag	gag	gac	tac	atc	gtc	tac	ctg	ggc	cgc	tca			1104
Ile	Asp	Tyr	Pro	Lys	Lys	Glu	Asp	Tyr	Ile	Val	Tyr	Leu	Gly	Arg	Ser			
		355				360						365						
agg	ctt	aac	tcc	aac	acg	caa	ggg	gag	atg	aag	ttt	gag	gtg	gaa	aac			1152
Arg	Leu	Asn	Ser	Asn	Thr	Gln	Gly	Glu	Met	Lys	Phe	Glu	Val	Glu	Asn			
	370					375					380							
ctc	atc	cta	cac	aag	gac	tac	agc	gct	gac	acg	ctt	gct	cac	cac	aac			1200
Leu	Ile	Leu	His	Lys	Asp	Tyr	Ser	Ala	Asp	Thr	Leu	Ala	His	His	Asn			

385	390	395	400	
gac att gcc ttg ctg aag atc cgt tcc aag gag ggc agg tgt gcg cag				1248
Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln	405	410	415	
cca tcc cgg act ata cag acc atc tgc ctg ccc tcg atg tat aac gat				1296
Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp	420	425	430	
ccc cag ttt ggc aca agc tgt gag atc act ggc ttt gga aaa gag aat				1344
Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn	435	440	445	
tct acc gac tat ctc tat ccg gag cag ctg aaa atg act gtt gtg aag				1392
Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys	450	455	460	
ctg att tcc cac cgg gag tgt cag cag ccc cac tac tac ggc tct gaa				1440
Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu	465	470	475	480
gtc acc acc aaa atg ctg tgt gct gct gac cca cag tgg aaa aca gat				1488
Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp	485	490	495	
tcc tgc cag gga gac tca ggg gga ccc ctc gtc tgt tcc ctc caa ggc				1536
Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly	500	505	510	
cgc atg act ttg act gga att gtg agc tgg ggc cgt gga tgt gcc ctg				1584
Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu	515	520	525	
aag gac aag cca ggc gtc tac acg aga gtc tca cac ttc tta ccc tgg				1632
Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp	530	535	540	
atc cgc agt cac acc aag gaa gag aat ggc ctg gcc ctc				1671
Ile Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu	545	550	555	

<210> 7

<211> 1674

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1) ... (837)

<223> Coding sequence of human SP-B precursor lacking the C-terminal propeptide

<220>

<221> CDS

<222> (838) ... (846)

<223> Linker sequence

<220>

<221> CDS

<222> (847) ... (1674)

<223> Coding sequence of low mw two-chain urokinase-plasminogen activator

<400> 7

atg gct gag tca cac ctg ctg cag tgg ctg ctg ctg ctg ctg ccc acg	48
Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr	
1 5 10 15	
ctc tgt ggc cca ggc act gct gcc tgg acc acc tca tcc ttg gcc tgt	96
Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys	
20 25 30	
gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag caa gca ttg cag	144
Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln	
35 40 45	
tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga	192
Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly	
50 55 60	
gcc gat gac cta tgc caa gag tgt gag gac atc gtc cac atc ctt aac	240
Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn	
65 70 75 80	
aag atg gcc aag gag gcc att ttc cag gac acg atg agg aag ttc ctg	288
Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu	
85 90 95	
gag cag gag tgc aac gtc ctc ccc ttg aag ctg ctc atg ccc cag tgc	336
Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys	
100 105 110	
aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag	384
Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln	
115 120 125	
aac cag act gac tca aac ggc atc tgt atg cac ctg ggc ctg tgc aaa	432
Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys	
130 135 140	
tcc cgg cag cca gag cca gag cag gag cca ggg atg tca gac ccc ctg	480
Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu	
145 150 155 160	
ccc aaa cct ctg cgg gac cct ctg cca gac cct ctg ctg gac aag ctc	528
Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu	
165 170 175	
gtc ctc cct gtg ctg ccc ggg gcc ctc cag gcg agg cct ggg cct cac	576
Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His	

180						185						190						
aca	cag	gat	ctc	tcc	gag	cag	caa	ttc	ccc	att	cct	ctc	ccc	tat	tgc	624		
Thr	Gln	Asp	Leu	Ser	Glu	Gln	Gln	Phe	Pro	Ile	Pro	Leu	Pro	Tyr	Cys			
195						200						205						
tgg	ctc	tgc	agg	gct	ctg	atc	aag	cgg	atc	caa	gcc	atg	att	ccc	aag	672		
Trp	Leu	Cys	Arg	Ala	Leu	Ile	Lys	Arg	Ile	Gln	Ala	Met	Ile	Pro	Lys			
210						215						220						
ggt	gcg	cta	gct	gtg	gca	gtg	gcc	cag	gtg	tgc	cgc	gtg	gta	cct	ctg	720		
Gly	Ala	Leu	Ala	Val	Ala	Val	Ala	Gln	Val	Cys	Arg	Val	Val	Pro	Leu			
225						230						235			240			
gtg	gcg	ggc	ggc	atc	tgc	cag	tgc	ctg	gct	gag	cgc	tac	tcc	gtc	atc	768		
Val	Ala	Gly	Gly	Ile	Cys	Gln	Cys	Leu	Ala	Glu	Arg	Tyr	Ser	Val	Ile			
			245						250						255			
ctg	ctc	gac	acg	ctg	ctg	ggc	cgc	atg	ctg	ccc	cag	ctg	gtc	tgc	cgc	816		
Leu	Leu	Asp	Thr	Leu	Leu	Gly	Arg	Met	Leu	Pro	Gln	Leu	Val	Cys	Arg			
			260						265						270			
ctc	gtc	ctc	cgg	tgc	tcc	atg	cag	ata	tct	aag	ccc	tcc	tct	cct	cca	864		
Leu	Val	Leu	Arg	Cys	Ser	Met	Gln	Ile	Ser	Lys	Pro	Ser	Ser	Pro	Pro			
275						280						285						
gaa	gaa	tta	aaa	ttt	cag	tgt	ggc	caa	aag	act	ctg	agg	ccc	cgc	ttt	912		
Glu	Glu	Leu	Lys	Phe	Gln	Cys	Gly	Gln	Lys	Thr	Leu	Arg	Pro	Arg	Phe			
290						295						300						
aag	att	att	ggg	gga	gaa	ttc	acc	acc	atc	gag	aac	cag	ccc	tgg	ttt	960		
Lys	Ile	Ile	Gly	Gly	Glu	Phe	Thr	Thr	Ile	Glu	Asn	Gln	Pro	Trp	Phe			
305						310						315			320			
gcg	gcc	atc	tac	agg	agg	cac	cgg	ggg	ggc	tct	gtc	acc	tac	gtg	tgt	1008		
Ala	Ala	Ile	Tyr	Arg	Arg	His	Arg	Gly	Gly	Ser	Val	Thr	Tyr	Val	Cys			
			325						330						335			
gga	ggc	agc	ctc	atc	agc	cct	tgc	tgg	gtg	atc	agc	gcc	aca	cac	tgc	1056		
Gly	Gly	Ser	Leu	Ile	Ser	Pro	Cys	Trp	Val	Ile	Ser	Ala	Thr	His	Cys			
			340						345						350			
ttc	att	gat	tac	cca	aag	aag	gag	gac	tac	atc	gtc	tac	ctg	ggt	cgc	1104		
Phe	Ile	Asp	Tyr	Pro	Lys	Lys	Glu	Asp	Tyr	Ile	Val	Tyr	Leu	Gly	Arg			
355						360						365						
tca	agg	ctt	aac	tcc	aac	acg	caa	ggg	gag	atg	aag	ttt	gag	gtg	gaa	1152		
Ser	Arg	Leu	Asn	Ser	Asn	Thr	Gln	Gly	Glu	Met	Lys	Phe	Glu	Val	Glu			
370						375						380						
aac	ctc	atc	cta	cac	aag	gac	tac	agc	gct	gac	acg	ctt	gct	cac	cac	1200		
Asn	Leu	Ile	Leu	His	Lys	Asp	Tyr	Ser	Ala	Asp	Thr	Leu	Ala	His	His			
385						390						395			400			
aac	gac	att	gcc	ttg	ctg	aag	atc	cgt	tcc	aag	gag	ggc	agg	tgt	gcg	1248		
Asn	Asp	Ile	Ala	Leu	Leu	Lys	Ile	Arg	Ser	Lys	Glu	Gly	Arg	Cys	Ala			
			405						410						415			

cag cca tcc cgg act ata cag acc atc tgc ctg ccc tcg atg tat aac	1296
Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn	
420 425 430	

gat ccc cag ttt ggc aca agc tgt gag atc act ggc ttt gga aaa gag	1344
Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu	
435 440 445	

aat tct acc gac tat ctc tat ccg gag cag ctg aaa atg act gtt gtg	1392
Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val	
450 455 460	

aag ctg att tcc cac cgg gag tgt cag cag ccc cac tac tac ggc tct	1440
Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser	
465 470 475 480	

gaa gtc acc acc aaa atg ctg tgt gct gct gac cca cag tgg aaa aca	1488
Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr	
485 490 495	

gat tcc tgc cag gga gac tca ggg gga ccc ctc gtc tgt tcc ctc caa	1536
Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln	
500 505 510	

ggc cgc atg act ttg act gga att gtg agc tgg ggc cgt gga tgt gcc	1584
Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala	
515 520 525	

ctg aag gac aag cca ggc gtc tac acg aga gtc tca cac ttc tta ccc	1632
Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro	
530 535 540	

tgg atc cgc agt cac acc aag gaa gag aat ggc ctg gcc ctc	1674
Trp Ile Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu	
545 550 555	

<210> 8  
 <211> 591  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1) ... (591)  
 <223> Coding sequence of the surfactant protein C precursor

<400> 8

atg gat gtg ggc agc aaa gag gtc ctg atg gag agc ccg ccg gac tac	48
Met Asp Val Gly Ser Lys Glu Val Leu Met Glu Ser Pro Pro Asp Tyr	
1 5 10 15	

tcc gca gct ccc cgg ggc cga ttt ggc att ccc tgc tgc cca gtg cac	96
Ser Ala Ala Pro Arg Gly Arg Phe Gly Ile Pro Cys Cys Pro Val His	
20 25 30	

ctg aaa cgc ctt ctt atc gtg gtg gtg gtg gtg gtc ctc atc gtc gtg Leu Lys Arg Leu Leu Ile Val Val Val Val Val Val Leu Ile Val Val	144
35 40 45	
gtg att gtg gga gcc ctg ctc atg ggt ctc cac atg agc cag aaa cac Val Ile Val Gly Ala Leu Leu Met Gly Leu His Met Ser Gln Lys His	192
50 55 60	
acg gag atg gtt ctg gag atg agc att ggg gcg ccg gaa gcc cag caa Thr Glu Met Val Leu Glu Met Ser Ile Gly Ala Pro Glu Ala Gln Gln	240
65 70 75 80	
cgc ctg gcc ctg agt gag cac ctg gtt acc act gcc acc ttc tcc atc Arg Leu Ala Leu Ser Glu His Leu Val Thr Thr Ala Thr Phe Ser Ile	288
85 90 95	
ggc tcc act ggc ctc gtg gtg tat gac tac cag cag ctg ctg atc gcc Gly Ser Thr Gly Leu Val Val Tyr Asp Tyr Gln Gln Leu Leu Ile Ala	336
100 105 110	
tac aag cca gcc cct ggc acc tgc tgc tac atc atg aag ata gct cca Tyr Lys Pro Ala Pro Gly Thr Cys Cys Tyr Ile Met Lys Ile Ala Pro	384
115 120 125	
gag agc atc ccc agt ctt gag gct ctc act aga aaa gtc cac aac ttc Glu Ser Ile Pro Ser Leu Glu Ala Leu Thr Arg Lys Val His Asn Phe	432
130 135 140	
cag atg gaa tgc tct ctg cag gcc aag ccc gca gtg cct acg tct aag Gln Met Glu Cys Ser Leu Gln Ala Lys Pro Ala Val Pro Thr Ser Lys	480
145 150 155 160	
ctg ggc cag gca gag ggg cga gat gca ggc tca gca ccc tcc gga ggg Leu Gly Gln Ala Glu Gly Arg Asp Ala Gly Ser Ala Pro Ser Gly Gly	528
165 170 175	
gac ccg gcc ttc ctg ggc atg gcc gtg agc acc ctg tgt ggc gag gtg Asp Pro Ala Phe Leu Gly Met Ala Val Ser Thr Leu Cys Gly Glu Val	576
180 185 190	
ccg ctc tac tac atc Pro Leu Tyr Tyr Ile	591
195	

<210> 9

<211> 174

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (174)

<223> Coding sequence of SP-C precursor lacking the C-terminal propeptide

<400> 9



atg	gat	gtg	ggc	agc	aaa	gag	gtc	ctg	atg	gag	agc	ccg	ccg	gac	tac	48
Met	Asp	Val	Gly	Ser	Lys	Glu	Val	Leu	Met	Glu	Ser	Pro	Pro	Asp	Tyr	
1				5				10						15		

tcc	gca	gct	ccc	cgg	ggc	cga	ttt	ggc	att	ccc	tgc	tgc	cca	gtg	cac	96
Ser	Ala	Ala	Pro	Arg	Gly	Arg	Phe	Gly	Ile	Pro	Cys	Cys	Pro	Val	His	
			20					25					30			

ctg	aaa	cgc	ctt	ctt	atc	gtg	gtg	gtg	gtg	gtg	gtc	ctc	atc	gtc	gtg	144
Leu	Lys	Arg	Leu	Leu	Ile	Val	Val	Val	Val	Val	Val	Leu	Ile	Val	Val	
		35					40					45				

gtg	att	gtg	gga	gcc	ctg	ctc	atg	ggt	ctc							174
Val	Ile	Val	Gly	Ala	Leu	Leu	Met	Gly	Leu							
	50					55										

<210> 10  
 <211> 105  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1) ... (105)  
 <223> Coding sequence of the mature surfactant protein C

<400> 10

ttt	ggc	att	ccc	tgc	tgc	cca	gtg	cac	ctg	aaa	cgc	ctt	ctt	atc	gtg	48
Phe	Gly	Ile	Pro	Cys	Cys	Pro	Val	His	Leu	Lys	Arg	Leu	Leu	Ile	Val	
1				5				10						15		

gtg	gtg	gtg	gtg	gtc	ctc	atc	gtc	gtg	gtg	att	gtg	gga	gcc	ctg	ctc	96
Val	Val	Val	Val	Val	Leu	Ile	Val	Val	Val	Ile	Val	Gly	Ala	Leu	Leu	
			20					25					30			

atg	ggt	ctc														105
Met	Gly	Leu														
		35														

<210> 11  
 <211> 1686  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1) ... (1686)  
 <223> Coding sequence of the tissue-plasminogen activator

<400> 11

atg	gat	gca	atg	aag	aga	ggg	ctc	tgc	tgt	gtg	ctg	ctg	ctg	tgt	gga	48
Met	Asp	Ala	Met	Lys	Arg	Gly	Leu	Cys	Cys	Val	Leu	Leu	Leu	Cys	Gly	

1	5	10	15	
gca gtc ttc gtt tcg ccc agc cag gaa atc cat gcc cga ttc aga aga				96
Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe Arg Arg	20	25	30	
gga gcc aga tct tac caa gtg atc tgc aga gat gaa aaa acg cag atg				144
Gly Ala Arg Ser Tyr Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met	35	40	45	
ata tac cag caa cat cag tca tgg ctg cgc cct gtg ctc aga agc aac				192
Ile Tyr Gln Gln His Gln Ser Trp Leu Arg Pro Val Leu Arg Ser Asn	50	55	60	
cgg gtg gaa tat tgc tgg tgc aac agt ggc agg gca cag tgc cac tca				240
Arg Val Glu Tyr Cys Trp Cys Asn Ser Gly Arg Ala Gln Cys His Ser	65	70	75	80
gtg cct gtc aaa agt tgc agc gag cca agg tgt ttc aac ggg ggc acc				288
Val Pro Val Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn Gly Gly Thr	85	90	95	
tgc cag cag gcc ctg tac ttc tca gat ttc gtg tgc cag tgc ccc gaa				336
Cys Gln Gln Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro Glu	100	105	110	
gga ttt gct ggg aag tgc tgt gaa ata gat acc agg gcc acg tgc tac				384
Gly Phe Ala Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr	115	120	125	
gag gac cag ggc atc agc tac agg ggc acg tgg agc aca gcg gag agt				432
Glu Asp Gln Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser	130	135	140	
ggc gcc gag tgc acc aac tgg aac agc agc gcg ttg gcc cag aag ccc				480
Gly Ala Glu Cys Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro	145	150	155	160
tac agc ggg cgg agg cca gat gcc atc agg ctg ggc ctg ggg aac cac				528
Tyr Ser Gly Arg Arg Pro Asp Ala Ile Arg Leu Gly Leu Gly Asn His	165	170	175	
aac tac tgc aga aac cca gat cga gac tca aag ccc tgg tgc tac gtc				576
Asn Tyr Cys Arg Asn Pro Asp Arg Asp Ser Lys Pro Trp Cys Tyr Val	180	185	190	
ttt aag gcg ggg aag tac agc tca gag ttc tgc agc acc cct gcc tgc				624
Phe Lys Ala Gly Lys Tyr Ser Ser Glu Phe Cys Ser Thr Pro Ala Cys	195	200	205	
tct gag gga aac agt gac tgc tac ttt ggg aat ggg tca gcc tac cgt				672
Ser Glu Gly Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr Arg	210	215	220	
ggc acg cac agc ctc acc gag tcg ggt gcc tcc tgc ctc ccg tgg aat				720
Gly Thr His Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn	225	230	235	240

tcc atg atc ctg ata ggc aag gtt tac aca gca cag aac ccc agt gcc Ser Met Ile Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala 245 250 255	768
cag gca ctg ggc ctg ggc aaa cat aat tac tgc cgg aat cct gat ggg Gln Ala Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly 260 265 270	816
gat gcc aag ccc tgg tgc cac gtg ctg aag aac cgc agg ctg acg tgg Asp Ala Lys Pro Trp Cys His Val Leu Lys Asn Arg Arg Leu Thr Trp 275 280 285	864
gag tac tgt gat gtg ccc tcc tgc tcc acc tgc ggc ctg aga cag tac Glu Tyr Cys Asp Val Pro Ser Cys Ser Thr Cys Gly Leu Arg Gln Tyr 290 295 300	912
agc cag cct cag ttt cgc atc aaa gga ggg ctc ttc gcc gac atc gcc Ser Gln Pro Gln Phe Arg Ile Lys Gly Gly Leu Phe Ala Asp Ile Ala 305 310 315 320	960
tcc cac ccc tgg cag gct gcc atc ttt gcc aag cac agg agg tcg ccc Ser His Pro Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser Pro 325 330 335	1008
gga gag cgg ttc ctg tgc ggg ggc ata ctc atc agc tcc tgc tgg att Gly Glu Arg Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp Ile 340 345 350	1056
ctc tct gcc gcc cac tgc ttc cag gag agg ttt ccg ccc cac cac ctg Leu Ser Ala Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu 355 360 365	1104
acg gtg atc ttg ggc aga aca tac cgg gtg gtc cct ggc gag gag gag Thr Val Ile Leu Gly Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Glu 370 375 380	1152
cag aaa ttt gaa gtc gaa aaa tac att gtc cat aag gaa ttc gat gat Gln Lys Phe Glu Val Glu Lys Tyr Ile Val His Lys Glu Phe Asp Asp 385 390 395 400	1200
gac act tac gac aat gac att gcg ctg ctg cag ctg aaa tcg gat tcg Asp Thr Tyr Asp Asn Asp Ile Ala Leu Leu Gln Leu Lys Ser Asp Ser 405 410 415	1248
tcc cgc tgt gcc cag gag agc agc gtg gtc cgc act gtg tgc ctt ccc Ser Arg Cys Ala Gln Glu Ser Ser Val Val Arg Thr Val Cys Leu Pro 420 425 430	1296
ccg gcg gac ctg cag ctg ccg gac tgg acg gag tgt gag ctc tcc ggc Pro Ala Asp Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu Leu Ser Gly 435 440 445	1344
tac ggc aag cat gag gcc ttg tct cct ttc tat tcg gag cgg ctg aag Tyr Gly Lys His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys 450 455 460	1392

[illegible]

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<210> 12
<211> 1158
<212> DNA
<213> Artificial Sequence
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<220>  
<221> sig_peptide  
<222> (1) ... (69)  
<223> Signal sequence of the human surfactant protein B
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<220>
<221> CDS
<222> (70) ... (75)
<223> Linker sequence
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```
<220>  
<221> CDS  
<222> (76) ... (312)  
<223> Coding sequence of the mature human surfactant protein B
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<220>
<221> CDS
<222> (313) ... (1140)
<223> Coding sequence of human low mw two-chain urokinase-plasminogen
activator
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<220>  
<221> CDS  
<222> (1141) ... (1158)
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<223> Hexahistidine affinity tag

<400> 12

atg gct gag tca cac ctg ctg cag tgg ctg ctg ctg ctg ctg ccc acg	48
Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr	
1 5 10 15	
ctc tgt ggc cca ggc act gct gcc tgg ttc ccc att cct ctc ccc tat	96
Leu Cys Gly Pro Gly Thr Ala Ala Trp Phe Pro Ile Pro Leu Pro Tyr	
20 25 30	
tgc tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att ccc	144
Cys Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro	
35 40 45	
aag ggt gcg cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta cct	192
Lys Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro	
50 55 60	
ctg gtg gcg ggc ggc atc tgc cag tgc ctg gct gag cgc tac tcc gtc	240
Leu Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val	
65 70 75 80	
atc ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc tgc	288
Ile Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys	
85 90 95	
cgc ctc gtc ctc cgg tgc tcc atg aag ccc tcc tct cct cca gaa gaa	336
Arg Leu Val Leu Arg Cys Ser Met Lys Pro Ser Ser Pro Pro Glu Glu	
100 105 110	
tta aaa ttt cag tgt ggc caa aag act ctg agg ccc cgc ttt aag att	384
Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile	
115 120 125	
att ggg gga gaa ttc acc acc atc gag aac cag ccc tgg ttt gcg gcc	432
Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala Ala	
130 135 140	
atc tac agg agg cac cgg ggg ggc tct gtc acc tac gtg tgt gga ggc	480
Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly	
145 150 155 160	
agc ctc atc agc cct tgc tgg gtg atc agc gcc aca cac tgc ttc att	528
Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile	
165 170 175	
gat tac cca aag aag gag gac tac atc gtc tac ctg ggt cgc tca agg	576
Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg	
180 185 190	
ctt aac tcc aac acg caa ggg gag atg aag ttt gag gtg gaa aac ctc	624
Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu	
195 200 205	
atc cta cac aag gac tac agc gct gac acg ctt gct cac cac aac gac	672

Ile	Leu	His	Lys	Asp	Tyr	Ser	Ala	Asp	Thr	Leu	Ala	His	His	Asn	Asp		
210						215					220						
att gcc ttg ctg aag atc cgt tcc aag gag ggc agg tgt gcg cag cca																	720
Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro						230				235						240	
225																	
tcc cgg act ata cag acc atc tgc ctg ccc tcg atg tat aac gat ccc																	768
Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro						245				250					255		
225																	
cag ttt ggc aca agc tgt gag atc act ggc ttt gga aaa gag aat tct																	816
Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser						260				265					270		
225																	
acc gac tat ctc tat ccg gag cag ctg aaa atg act gtt gtg aag ctg																	864
Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu						275				280				285			
225																	
att tcc cac cgg gag tgt cag cag ccc cac tac tac ggc tct gaa gtc																	912
Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val						290				295				300			
225																	
acc acc aaa atg ctg tgt gct gct gac cca cag tgg aaa aca gat tcc																	960
Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser						305				310				315		320	
225																	
tgc cag gga gac tca ggg gga ccc ctc gtc tgt tcc ctc caa ggc cgc																	1008
Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg						325				330				335			
225																	
atg act ttg act gga att gtg agc tgg ggc cgt gga tgt gcc ctg aag																	1056
Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys						340				345				350			
225																	
gac aag cca ggc gtc tac acg aga gtc tca cac ttc tta ccc tgg atc																	1104
Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile						355				360				365			
225																	
cgc agt cac acc aag gaa gag aat ggc ctg gcc ctc cat cat cat cat																	1152
Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu His His His His						370				375				380			
225																	
cat cat																	1158
His His																	
385																	

<210> 13  
 <211> 1149  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> sig\_peptide  
 <222> (1) ... (60)  
 <223> Signal sequence of the human urokinase plasminogen activator

<220>  
 <221> CDS  
 <222> (61) ... (66)  
 <223> Linker sequence

<220>  
 <221> CDS  
 <222> (67) ... (894)  
 <223> Coding sequence of human low mw two-chain urokinase-plasminogen activator

<220>  
 <221> CDS  
 <222> (895) ... (1131)  
 <223> Coding sequence of the mature human surfactant protein B

<220>  
 <221> CDS  
 <222> (1132) ... (1149)  
 <223> Hexahistidin affinity tag

<400> 13

atg aga gcc ctg ctg gcg cgc ctg ctt ctc tgc gtc ctg gtc gtg agc	48
Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser	
1 5 10 15	
gac tcc aaa ggc agc aat aag ccc tcc tct cct cca gaa gaa tta aaa	96
Asp Ser Lys Gly Ser Asn Lys Pro Ser Ser Pro Pro Glu Glu Leu Lys	
20 25 30	
ttt cag tgt ggc caa aag act ctg agg ccc cgc ttt aag att att ggg	144
Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile Gly	
35 40 45	
gga gaa ttc acc acc atc gag aac cag ccc tgg ttt gcg gcc atc tac	192
Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala Ala Ile Tyr	
50 55 60	
agg agg cac cgg ggg ggc tct gtc acc tac gtg tgt gga ggc agc ctc	240
Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser Leu	
65 70 75 80	
atc agc cct tgc tgg gtg atc agc gcc aca cac tgc ttc att gat tac	288
Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp Tyr	
85 90 95	
cca aag aag gag gac tac atc gtc tac ctg ggt cgc tca agg ctt aac	336
Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Leu Asn	
100 105 110	
tcc aac acg caa ggg gag atg aag ttt gag gtg gaa aac ctc atc cta	384
Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Ile Leu	
115 120 125	
cac aag gac tac agc gct gac acg ctt gct cac cac aac gac att gcc	432



His	Lys	Asp	Tyr	Ser	Ala	Asp	Thr	Leu	Ala	His	His	Asn	Asp	Ile	Ala	
130						135				140						
ttg	ctg	aag	atc	cgt	tcc	aag	gag	ggc	agg	tgt	gcg	cag	cca	tcc	cgg	480
Leu	Leu	Lys	Ile	Arg	Ser	Lys	Glu	Gly	Arg	Cys	Ala	Gln	Pro	Ser	Arg	
145					150					155					160	
act	ata	cag	acc	atc	tgc	ctg	ccc	tcg	atg	tat	aac	gat	ccc	cag	ttt	528
Thr	Ile	Gln	Thr	Ile	Cys	Leu	Pro	Ser	Met	Tyr	Asn	Asp	Pro	Gln	Phe	
				165					170					175		
ggc	aca	agc	tgt	gag	atc	act	ggc	ttt	gga	aaa	gag	aat	tct	acc	gac	576
Gly	Thr	Ser	Cys	Glu	Ile	Thr	Gly	Phe	Gly	Lys	Glu	Asn	Ser	Thr	Asp	
			180					185					190			
tat	ctc	tat	ccg	gag	cag	ctg	aaa	atg	act	gtt	gtg	aag	ctg	att	tcc	624
Tyr	Leu	Tyr	Pro	Glu	Gln	Leu	Lys	Met	Thr	Val	Val	Lys	Leu	Ile	Ser	
		195					200					205				
cac	cgg	gag	tgt	cag	cag	ccc	cac	tac	tac	ggc	tct	gaa	gtc	acc	acc	672
His	Arg	Glu	Cys	Gln	Gln	Pro	His	Tyr	Tyr	Gly	Ser	Glu	Val	Thr	Thr	
	210					215					220					
aaa	atg	ctg	tgt	gct	gct	gac	cca	cag	tgg	aaa	aca	gat	tcc	tgc	cag	720
Lys	Met	Leu	Cys	Ala	Ala	Asp	Pro	Gln	Trp	Lys	Thr	Asp	Ser	Cys	Gln	
225					230					235					240	
gga	gac	tca	ggg	gga	ccc	ctc	gtc	tgt	tcc	ctc	caa	ggc	cgc	atg	act	768
Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Ser	Leu	Gln	Gly	Arg	Met	Thr	
				245					250					255		
ttg	act	gga	att	gtg	agc	tgg	ggc	cgt	gga	tgt	gcc	ctg	aag	gac	aag	816
Leu	Thr	Gly	Ile	Val	Ser	Trp	Gly	Arg	Gly	Cys	Ala	Leu	Lys	Asp	Lys	
			260					265					270			
cca	ggc	gtc	tac	acg	aga	gtc	tca	cac	ttc	tta	ccc	tgg	atc	cgc	agt	864
Pro	Gly	Val	Tyr	Thr	Arg	Val	Ser	His	Phe	Leu	Pro	Trp	Ile	Arg	Ser	
		275					280					285				
cac	acc	aag	gaa	gag	aat	ggc	ctg	gcc	ctc	ttc	ccc	att	cct	ctc	ccc	912
His	Thr	Lys	Glu	Gln	Asn	Gly	Leu	Ala	Leu	Phe	Pro	Ile	Pro	Leu	Pro	
	290					295					300					
tat	tgc	tgg	ctc	tgc	agg	gct	ctg	atc	aag	cgg	atc	caa	gcc	atg	att	960
Tyr	Cys	Trp	Leu	Cys	Arg	Ala	Leu	Ile	Lys	Arg	Ile	Gln	Ala	Met	Ile	
305					310					315					320	
ccc	aag	ggt	gcg	cta	gct	gtg	gca	gtg	gcc	cag	gtg	tgc	cgc	gtg	gta	1008
Pro	Lys	Gly	Ala	Leu	Ala	Val	Ala	Val	Ala	Gln	Val	Cys	Arg	Val	Val	
				325					330					335		
cct	ctg	gtg	gcg	ggc	ggc	atc	tgc	cag	tgc	ctg	gct	gag	cgc	tac	tcc	1056
Pro	Leu	Val	Ala	Gly	Gly	Ile	Cys	Gln	Cys	Leu	Ala	Glu	Arg	Tyr	Ser	
			340					345					350			
gtc	atc	ctg	ctc	gac	acg	ctg	ctg	ggc	cgc	atg	ctg	ccc	cag	ctg	gtc	1104
Val	Ile	Leu	Leu	Asp	Thr	Leu	Leu	Gly	Arg	Met	Leu	Pro	Gln	Leu	Val	

355	360	365	
tgc cgc ctc gtc ctc cgg tgc tcc atg cat cat cat cat cat cat			1149
Cys Arg Leu Val Leu Arg Cys Ser Met His His His His His His			
370	375	380	

<210> 14  
 <211> 381  
 <212> PRT  
 <213> Homo sapiens  
  
 <220>  
  
 <221> PEPTIDE  
 <222> (1) ... (381)  
 <223> Surfactant protein B precursor  
  
 <400> 14

Met	Ala	Glu	Ser	His	Leu	Leu	Gln	Trp	Leu	Leu	Leu	Leu	Leu	Pro	Thr
1				5					10					15	
Leu	Cys	Gly	Pro	Gly	Thr	Ala	Ala	Trp	Thr	Thr	Ser	Ser	Leu	Ala	Cys
			20					25					30		
Ala	Gln	Gly	Pro	Glu	Phe	Trp	Cys	Gln	Ser	Leu	Glu	Gln	Ala	Leu	Gln
		35					40					45			
Cys	Arg	Ala	Leu	Gly	His	Cys	Leu	Gln	Glu	Val	Trp	Gly	His	Val	Gly
	50					55					60				
Ala	Asp	Asp	Leu	Cys	Gln	Glu	Cys	Glu	Asp	Ile	Val	His	Ile	Leu	Asn
65					70					75					80
Lys	Met	Ala	Lys	Glu	Ala	Ile	Phe	Gln	Asp	Thr	Met	Arg	Lys	Phe	Leu
				85					90					95	
Glu	Gln	Glu	Cys	Asn	Val	Leu	Pro	Leu	Lys	Leu	Leu	Met	Pro	Gln	Cys
			100					105					110		
Asn	Gln	Val	Leu	Asp	Asp	Tyr	Phe	Pro	Leu	Val	Ile	Asp	Tyr	Phe	Gln
		115					120					125			
Asn	Gln	Thr	Asp	Ser	Asn	Gly	Ile	Cys	Met	His	Leu	Gly	Leu	Cys	Lys
		130				135					140				
Ser	Arg	Gln	Pro	Glu	Pro	Glu	Gln	Glu	Pro	Gly	Met	Ser	Asp	Pro	Leu
145					150					155					160
Pro	Lys	Pro	Leu	Arg	Asp	Pro	Leu	Pro	Asp	Pro	Leu	Leu	Asp	Lys	Leu
				165					170					175	
Val	Leu	Pro	Val	Leu	Pro	Gly	Ala	Leu	Gln	Ala	Arg	Pro	Gly	Pro	His
			180					185					190		

Thr	Gln	Asp	Leu	Ser	Glu	Gln	Gln	Phe	Pro	Ile	Pro	Leu	Pro	Tyr	Cys	
		195					200					205				
Trp	Leu	Cys	Arg	Ala	Leu	Ile	Lys	Arg	Ile	Gln	Ala	Met	Ile	Pro	Lys	
	210					215					220					
Gly	Ala	Leu	Ala	Val	Ala	Val	Ala	Gln	Val	Cys	Arg	Val	Val	Pro	Leu	
225					230					235					240	
Val	Ala	Gly	Gly	Ile	Cys	Gln	Cys	Leu	Ala	Glu	Arg	Tyr	Ser	Val	Ile	
				245					250					255		
Leu	Leu	Asp	Thr	Leu	Leu	Gly	Arg	Met	Leu	Pro	Gln	Leu	Val	Cys	Arg	
			260					265					270			
Leu	Val	Leu	Arg	Cys	Ser	Met	Asp	Asp	Ser	Ala	Gly	Pro	Arg	Ser	Pro	
		275					280					285				
Thr	Gly	Glu	Trp	Leu	Pro	Arg	Asp	Ser	Glu	Cys	His	Leu	Cys	Met	Ser	
	290					295					300					
Val	Thr	Thr	Gln	Ala	Gly	Asn	Ser	Ser	Glu	Gln	Ala	Ile	Pro	Gln	Ala	
305					310					315					320	
Met	Leu	Gln	Ala	Cys	Val	Gly	Ser	Trp	Leu	Asp	Arg	Glu	Lys	Cys	Lys	
				325					330					335		
Gln	Phe	Val	Glu	Gln	His	Thr	Pro	Gln	Leu	Leu	Thr	Leu	Val	Pro	Arg	
			340					345					350			
Gly	Trp	Asp	Ala	His	Thr	Thr	Cys	Gln	Ala	Leu	Gly	Val	Cys	Gly	Thr	
		355					360					365				
Met	Ser	Ser	Pro	Leu	Gln	Cys	Ile	His	Ser	Pro	Asp	Leu				
	370					375					380					

<210> 15  
 <211> 279  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> PEPTIDE  
 <222> (1) ... (279)  
 <223> Surfactant protein B precursor lacking the C-terminal propeptide

<400> 15

Met	Ala	Glu	Ser	His	Leu	Leu	Gln	Trp	Leu	Leu	Leu	Leu	Leu	Pro	Thr	
1				5				10						15		
Leu	Cys	Gly	Pro	Gly	Thr	Ala	Ala	Trp	Thr	Thr	Ser	Ser	Leu	Ala	Cys	
			20					25					30			
Ala	Gln	Gly	Pro	Glu	Phe	Trp	Cys	Gln	Ser	Leu	Glu	Gln	Ala	Leu	Gln	
		35					40					45				



<223> Mature surfactant protein B

<400> 16

Phe	Pro	Ile	Pro	Leu	Pro	Tyr	Cys	Trp	Leu	Cys	Arg	Ala	Leu	Ile	Lys
1				5					10					15	
Arg	Ile	Gln	Ala	Met	Ile	Pro	Lys	Gly	Ala	Leu	Ala	Val	Ala	Val	Ala
			20					25					30		
Gln	Val	Cys	Arg	Val	Val	Pro	Leu	Val	Ala	Gly	Gly	Ile	Cys	Gln	Cys
		35					40					45			
Leu	Ala	Glu	Arg	Tyr	Ser	Val	Ile	Leu	Leu	Asp	Thr	Leu	Leu	Gly	Arg
	50					55					60				
Met	Leu	Pro	Gln	Leu	Val	Cys	Arg	Leu	Val	Leu	Arg	Cys	Ser	Met	
65					70					75					

<210> 17

<211> 431

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1) ... (431)

<223> Single-chain urokinase-plasminogen activator

<400> 17

Met	Arg	Ala	Leu	Leu	Ala	Arg	Leu	Leu	Leu	Cys	Val	Leu	Val	Val	Ser
1				5					10					15	
Asp	Ser	Lys	Gly	Ser	Asn	Glu	Leu	His	Gln	Val	Pro	Ser	Asn	Cys	Asp
			20					25					30		
Cys	Leu	Asn	Gly	Gly	Thr	Cys	Val	Ser	Asn	Lys	Tyr	Phe	Ser	Asn	Ile
		35					40					45			
His	Trp	Cys	Asn	Cys	Pro	Lys	Lys	Phe	Gly	Gly	Gln	His	Cys	Glu	Ile
	50					55					60				
Asp	Lys	Ser	Lys	Thr	Cys	Tyr	Glu	Gly	Asn	Gly	His	Phe	Tyr	Arg	Gly
65					70				75						80
Lys	Ala	Ser	Thr	Asp	Thr	Met	Gly	Arg	Pro	Cys	Leu	Pro	Trp	Asn	Ser
				85					90					95	
Ala	Thr	Val	Leu	Gln	Gln	Thr	Tyr	His	Ala	His	Arg	Ser	Asp	Ala	Leu
			100					105					110		
Gln	Leu	Gly	Leu	Gly	Lys	His	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Asn	Arg
		115					120					125			
Arg	Arg	Pro	Trp	Cys	Tyr	Val	Gln	Val	Gly	Leu	Lys	Pro	Leu	Val	Gln

130						135						140				
Glu	Cys	Met	Val	His	Asp	Cys	Ala	Asp	Gly	Lys	Lys	Pro	Ser	Ser	Pro	
145						150					155					160
Pro	Glu	Glu	Leu	Lys	Phe	Gln	Cys	Gly	Gln	Lys	Thr	Leu	Arg	Pro	Arg	
				165					170					175		
Phe	Lys	Ile	Ile	Gly	Gly	Glu	Phe	Thr	Thr	Ile	Glu	Asn	Gln	Pro	Trp	
			180					185					190			
Phe	Ala	Ala	Ile	Tyr	Arg	Arg	His	Arg	Gly	Gly	Ser	Val	Thr	Tyr	Val	
	195						200					205				
Cys	Gly	Gly	Ser	Leu	Ile	Ser	Pro	Cys	Trp	Val	Ile	Ser	Ala	Thr	His	
	210					215					220					
Cys	Phe	Ile	Asp	Tyr	Pro	Lys	Lys	Glu	Asp	Tyr	Ile	Val	Tyr	Leu	Gly	
225					230					235					240	
Arg	Ser	Arg	Leu	Asn	Ser	Asn	Thr	Gln	Gly	Glu	Met	Lys	Phe	Glu	Val	
				245					250					255		
Glu	Asn	Leu	Ile	Leu	His	Lys	Asp	Tyr	Ser	Ala	Asp	Thr	Leu	Ala	His	
			260					265					270			
His	Asn	Asp	Ile	Ala	Leu	Leu	Lys	Ile	Arg	Ser	Lys	Glu	Gly	Arg	Cys	
	275						280					285				
Ala	Gln	Pro	Ser	Arg	Thr	Ile	Gln	Thr	Ile	Cys	Leu	Pro	Ser	Met	Tyr	
	290					295					300					
Asn	Asp	Pro	Gln	Phe	Gly	Thr	Ser	Cys	Glu	Ile	Thr	Gly	Phe	Gly	Lys	
305					310					315					320	
Glu	Asn	Ser	Thr	Asp	Tyr	Leu	Tyr	Pro	Glu	Gln	Leu	Lys	Met	Thr	Val	
				325					330					335		
Val	Lys	Leu	Ile	Ser	His	Arg	Glu	Cys	Gln	Gln	Pro	His	Tyr	Tyr	Gly	
			340					345					350			
Ser	Glu	Val	Thr	Thr	Lys	Met	Leu	Cys	Ala	Ala	Asp	Pro	Gln	Trp	Lys	
	355						360					365				
Thr	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Ser	Leu	
	370					375					380					
Gln	Gly	Arg	Met	Thr	Leu	Thr	Gly	Ile	Val	Ser	Trp	Gly	Arg	Gly	Cys	
385					390					395					400	
Ala	Leu	Lys	Asp	Lys	Pro	Gly	Val	Tyr	Thr	Arg	Val	Ser	His	Phe	Leu	
				405					410					415		
Pro	Trp	Ile	Arg	Ser	His	Thr	Lys	Glu	Gln	Asn	Gly	Leu	Ala	Leu		
			420					425					430			

<210> 18  
 <211> 276  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> PEPTIDE  
 <222> (1) ... (276)  
 <223> Low molecular weight two-chain urokinase-plasminogen activator

<400> 18

Lys	Pro	Ser	Ser	Pro	Pro	Glu	Glu	Leu	Lys	Phe	Gln	Cys	Gly	Gln	Lys	1	5	10	15
Thr	Leu	Arg	Pro	Arg	Phe	Lys	Ile	Ile	Gly	Gly	Glu	Phe	Thr	Thr	Ile	20	25	30	
Glu	Asn	Gln	Pro	Trp	Phe	Ala	Ala	Ile	Tyr	Arg	Arg	His	Arg	Gly	Gly	35	40	45	
Ser	Val	Thr	Tyr	Val	Cys	Gly	Gly	Ser	Leu	Ile	Ser	Pro	Cys	Trp	Val	50	55	60	
Ile	Ser	Ala	Thr	His	Cys	Phe	Ile	Asp	Tyr	Pro	Lys	Lys	Glu	Asp	Tyr	65	70	75	80
Ile	Val	Tyr	Leu	Gly	Arg	Ser	Arg	Leu	Asn	Ser	Asn	Thr	Gln	Gly	Glu	85	90	95	
Met	Lys	Phe	Glu	Val	Glu	Asn	Leu	Ile	Leu	His	Lys	Asp	Tyr	Ser	Ala	100	105	110	
Asp	Thr	Leu	Ala	His	His	Asn	Asp	Ile	Ala	Leu	Leu	Lys	Ile	Arg	Ser	115	120	125	
Lys	Glu	Gly	Arg	Cys	Ala	Gln	Pro	Ser	Arg	Thr	Ile	Gln	Thr	Ile	Cys	130	135	140	
Leu	Pro	Ser	Met	Tyr	Asn	Asp	Pro	Gln	Phe	Gly	Thr	Ser	Cys	Glu	Ile	145	150	155	160
Thr	Gly	Phe	Gly	Lys	Glu	Asn	Ser	Thr	Asp	Tyr	Leu	Tyr	Pro	Glu	Gln	165	170	175	
Leu	Lys	Met	Thr	Val	Val	Lys	Leu	Ile	Ser	His	Arg	Glu	Cys	Gln	Gln	180	185	190	
Pro	His	Tyr	Tyr	Gly	Ser	Glu	Val	Thr	Thr	Lys	Met	Leu	Cys	Ala	Ala	195	200	205	
Asp	Pro	Gln	Trp	Lys	Thr	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	210	215	220	
Leu	Val	Cys	Ser	Leu	Gln	Gly	Arg	Met	Thr	Leu	Thr	Gly	Ile	Val	Ser	225	230	235	240



Trp Gly Arg Gly Cys Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg  
245 250 255

Val Ser His Phe Leu Pro Trp Ile Arg Ser His Thr Lys Glu Gln Asn  
260 265 270

Gly Leu Ala Leu  
275

<210> 19  
<211> 557  
<212> PRT  
<213> Artificial Sequence

<220>  
<221> PEPTIDE  
<222> (1) ... (279)  
<223> Human surfactant protein B precursor lacking the C-terminal  
propeptide

<220>  
<221> PEPTIDE  
<222> (280) ... (281)  
<223> Linker

<220>  
<221> PEPTIDE  
<222> (282) ... (557)  
<223> Human low molecular weight two-chain urokinase-plasminogen activator

<400> 19

Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Pro Thr  
1 5 10 15

Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys  
20 25 30

Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln  
35 40 45

Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly  
50 55 60

Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn  
65 70 75 80

Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu  
85 90 95

Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys  
100 105 110

Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln  
115 120 125

Asn	Gln	Thr	Asp	Ser	Asn	Gly	Ile	Cys	Met	His	Leu	Gly	Leu	Cys	Lys	130	135	140	
Ser	Arg	Gln	Pro	Glu	Pro	Glu	Gln	Glu	Pro	Gly	Met	Ser	Asp	Pro	Leu	145	150	155	160
Pro	Lys	Pro	Leu	Arg	Asp	Pro	Leu	Pro	Asp	Pro	Leu	Leu	Asp	Lys	Leu	165	170	175	
Val	Leu	Pro	Val	Leu	Pro	Gly	Ala	Leu	Gln	Ala	Arg	Pro	Gly	Pro	His	180	185	190	
Thr	Gln	Asp	Leu	Ser	Glu	Gln	Gln	Phe	Pro	Ile	Pro	Leu	Pro	Tyr	Cys	195	200	205	
Trp	Leu	Cys	Arg	Ala	Leu	Ile	Lys	Arg	Ile	Gln	Ala	Met	Ile	Pro	Lys	210	215	220	
Gly	Ala	Leu	Ala	Val	Ala	Val	Ala	Gln	Val	Cys	Arg	Val	Val	Pro	Leu	225	230	235	240
Val	Ala	Gly	Gly	Ile	Cys	Gln	Cys	Leu	Ala	Glu	Arg	Tyr	Ser	Val	Ile	245	250	255	
Leu	Leu	Asp	Thr	Leu	Leu	Gly	Arg	Met	Leu	Pro	Gln	Leu	Val	Cys	Arg	260	265	270	
Leu	Val	Leu	Arg	Cys	Ser	Met	Lys	Leu	Lys	Pro	Ser	Ser	Pro	Pro	Glu	275	280	285	
Glu	Leu	Lys	Phe	Gln	Cys	Gly	Gln	Lys	Thr	Leu	Arg	Pro	Arg	Phe	Lys	290	295	300	
Ile	Ile	Gly	Gly	Glu	Phe	Thr	Thr	Ile	Glu	Asn	Gln	Pro	Trp	Phe	Ala	305	310	315	320
Ala	Ile	Tyr	Arg	Arg	His	Arg	Gly	Gly	Ser	Val	Thr	Tyr	Val	Cys	Gly	325	330	335	
Gly	Ser	Leu	Ile	Ser	Pro	Cys	Trp	Val	Ile	Ser	Ala	Thr	His	Cys	Phe	340	345	350	
Ile	Asp	Tyr	Pro	Lys	Lys	Glu	Asp	Tyr	Ile	Val	Tyr	Leu	Gly	Arg	Ser	355	360	365	
Arg	Leu	Asn	Ser	Asn	Thr	Gln	Gly	Glu	Met	Lys	Phe	Glu	Val	Glu	Asn	370	375	380	
Leu	Ile	Leu	His	Lys	Asp	Tyr	Ser	Ala	Asp	Thr	Leu	Ala	His	His	Asn	385	390	395	400
Asp	Ile	Ala	Leu	Leu	Lys	Ile	Arg	Ser	Lys	Glu	Gly	Arg	Cys	Ala	Gln	405	410	415	
Pro	Ser	Arg	Thr	Ile	Gln	Thr	Ile	Cys	Leu	Pro	Ser	Met	Tyr	Asn	Asp	420	425	430	

Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn  
 435 440 445  
 Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys  
 450 455 460  
 Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu  
 465 470 475 480  
 Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp  
 485 490 495  
 Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly  
 500 505 510  
 Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu  
 515 520 525  
 Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp  
 530 535 540  
 Ile Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu  
 545 550 555

<210> 20  
 <211> 558  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <221> PEPTIDE  
 <222> (1) ... (279)  
 <223> Human surfactant protein B precursor lacking the C-terminal  
 propeptide

<220>  
 <221> PEPTIDE  
 <222> (280) ... (282)  
 <223> Linker

<220>  
 <221> PEPTIDE  
 <222> (283) ... (558)  
 <223> Human low molecular weight two-chain urokinase-plasminogen activator

<400> 20

Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Pro Thr  
 1 5 10 15  
 Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys  
 20 25 30  
 Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln  
 35 40 45

Cys	Arg	Ala	Leu	Gly	His	Cys	Leu	Gln	Glu	Val	Trp	Gly	His	Val	Gly		
	50					55					60						
Ala	Asp	Asp	Leu	Cys	Gln	Glu	Cys	Glu	Asp	Ile	Val	His	Ile	Leu	Asn		
	65				70					75					80		
Lys	Met	Ala	Lys	Glu	Ala	Ile	Phe	Gln	Asp	Thr	Met	Arg	Lys	Phe	Leu		
				85					90					95			
Glu	Gln	Glu	Cys	Asn	Val	Leu	Pro	Leu	Lys	Leu	Leu	Met	Pro	Gln	Cys		
			100					105					110				
Asn	Gln	Val	Leu	Asp	Asp	Tyr	Phe	Pro	Leu	Val	Ile	Asp	Tyr	Phe	Gln		
		115					120					125					
Asn	Gln	Thr	Asp	Ser	Asn	Gly	Ile	Cys	Met	His	Leu	Gly	Leu	Cys	Lys		
		130				135					140						
Ser	Arg	Gln	Pro	Glu	Pro	Glu	Gln	Glu	Pro	Gly	Met	Ser	Asp	Pro	Leu		
	145				150					155					160		
Pro	Lys	Pro	Leu	Arg	Asp	Pro	Leu	Pro	Asp	Pro	Leu	Leu	Asp	Lys	Leu		
				165					170					175			
Val	Leu	Pro	Val	Leu	Pro	Gly	Ala	Leu	Gln	Ala	Arg	Pro	Gly	Pro	His		
			180					185					190				
Thr	Gln	Asp	Leu	Ser	Glu	Gln	Gln	Phe	Pro	Ile	Pro	Leu	Pro	Tyr	Cys		
		195				200						205					
Trp	Leu	Cys	Arg	Ala	Leu	Ile	Lys	Arg	Ile	Gln	Ala	Met	Ile	Pro	Lys		
	210					215					220						
Gly	Ala	Leu	Ala	Val	Ala	Val	Ala	Gln	Val	Cys	Arg	Val	Val	Pro	Leu		
	225				230					235					240		
Val	Ala	Gly	Gly	Ile	Cys	Gln	Cys	Leu	Ala	Glu	Arg	Tyr	Ser	Val	Ile		
				245					250					255			
Leu	Leu	Asp	Thr	Leu	Leu	Gly	Arg	Met	Leu	Pro	Gln	Leu	Val	Cys	Arg		
			260					265					270				
Leu	Val	Leu	Arg	Cys	Ser	Met	Gln	Ile	Ser	Lys	Pro	Ser	Ser	Pro	Pro		
		275					280					285					
Glu	Glu	Leu	Lys	Phe	Gln	Cys	Gly	Gln	Lys	Thr	Leu	Arg	Pro	Arg	Phe		
	290					295					300						
Lys	Ile	Ile	Gly	Gly	Glu	Phe	Thr	Thr	Ile	Glu	Asn	Gln	Pro	Trp	Phe		
	305				310					315					320		
Ala	Ala	Ile	Tyr	Arg	Arg	His	Arg	Gly	Gly	Ser	Val	Thr	Tyr	Val	Cys		
				325					330					335			
Gly	Gly	Ser	Leu	Ile	Ser	Pro	Cys	Trp	Val	Ile	Ser	Ala	Thr	His	Cys		



Ser Ala Ala Pro Arg Gly Arg Phe Gly Ile Pro Cys Cys Pro Val His  
                   20                  25                  30  
 Leu Lys Arg Leu Leu Ile Val Val Val Val Val Val Leu Ile Val Val  
                   35                  40                  45  
 Val Ile Val Gly Ala Leu Leu Met Gly Leu His Met Ser Gln Lys His  
           50                  55                  60  
 Thr Glu Met Val Leu Glu Met Ser Ile Gly Ala Pro Glu Ala Gln Gln  
   65                  70                  75                  80  
 Arg Leu Ala Leu Ser Glu His Leu Val Thr Thr Ala Thr Phe Ser Ile  
                   85                  90                  95  
 Gly Ser Thr Gly Leu Val Val Tyr Asp Tyr Gln Gln Leu Leu Ile Ala  
                   100                  105                  110  
 Tyr Lys Pro Ala Pro Gly Thr Cys Cys Tyr Ile Met Lys Ile Ala Pro  
           115                  120                  125  
 Glu Ser Ile Pro Ser Leu Glu Ala Leu Thr Arg Lys Val His Asn Phe  
           130                  135                  140  
 Gln Met Glu Cys Ser Leu Gln Ala Lys Pro Ala Val Pro Thr Ser Lys  
   145                  150                  155                  160  
 Leu Gly Gln Ala Glu Gly Arg Asp Ala Gly Ser Ala Pro Ser Gly Gly  
                   165                  170                  175  
 Asp Pro Ala Phe Leu Gly Met Ala Val Ser Thr Leu Cys Gly Glu Val  
                   180                  185                  190  
 Pro Leu Tyr Tyr Ile  
           195

<210> 22  
 <211> 58  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> PEPTIDE  
 <222> (1) ... (58)  
 <223> Surfactant protein C precursor lacking the C-terminal  
           propeptide

<400> 22

Met Asp Val Gly Ser Lys Glu Val Leu Met Glu Ser Pro Pro Asp Tyr  
   1                  5                  10                  15  
 Ser Ala Ala Pro Arg Gly Arg Phe Gly Ile Pro Cys Cys Pro Val His  
                   20                  25                  30  
 Leu Lys Arg Leu Leu Ile Val Val Val Val Val Val Leu Ile Val Val

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      35              40              45
Val Ile Val Gly Ala Leu Leu Met Gly Leu
   50                55

<210> 23
<211> 35
<212> PRT
<213> Homo sapiens

<220>
<221> PEPTIDE
<222> (1) ... (35)
<223> Mature surfactant protein C

<400> 23

Phe Gly Ile Pro Cys Cys Pro Val His Leu Lys Arg Leu Leu Ile Val
  1          5             10           15

Val Val Val Val Val Leu Ile Val Val Val Ile Val Gly Ala Leu Leu
    20                25                 30

Met Gly Leu
     35


<210> 24
<211> 562
<212> PRT
<213> Homo sapiens

<220>
<221> PEPTIDE
<222> (1) ... (562)
<223> Tissue-plasminogen activator

<400> 24

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
  1          5             10           15

Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe Arg Arg
    20                25                 30

Gly Ala Arg Ser Tyr Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met
    35                40                 45

Ile Tyr Gln Gln His Gln Ser Trp Leu Arg Pro Val Leu Arg Ser Asn
  50          55             60

Arg Val Glu Tyr Cys Trp Cys Asn Ser Gly Arg Ala Gln Cys His Ser
  65          70             75           80

Val Pro Val Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn Gly Gly Thr
    85                90                 95
```





Asp Thr Tyr Asp Asn Asp Ile Ala Leu Leu Gln Leu Lys Ser Asp Ser  
 405 410 415  
 Ser Arg Cys Ala Gln Glu Ser Ser Val Val Arg Thr Val Cys Leu Pro  
 420 425 430  
 Pro Ala Asp Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu Leu Ser Gly  
 435 440 445  
 Tyr Gly Lys His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys  
 450 455 460  
 Glu Ala His Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His  
 465 470 475 480  
 Leu Leu Asn Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr  
 485 490 495  
 Arg Ser Gly Gly Pro Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp  
 500 505 510  
 Ser Gly Gly Pro Leu Val Cys Leu Asn Asp Gly Arg Met Thr Leu Val  
 515 520 525  
 Gly Ile Ile Ser Trp Gly Leu Gly Cys Gly Gln Lys Asp Val Pro Gly  
 530 535 540  
 Val Tyr Thr Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg Asp Asn Met  
 545 550 555 560

Arg Pro

<210> 25  
 <211> 386  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <221> SIGNAL  
 <222> (1) ... (23)  
 <223> Signal sequence of the human surfactant protein B

<220>  
 <221> PEPTIDE  
 <222> (24) ... (25)  
 <223> Linker

<220>  
 <221> PEPTIDE  
 <222> (26) ... (104)  
 <223> Mature human surfactant protein B

<220>  
 <221> PEPTIDE  
 <222> (105) ... (380)

<223> Human low molecular weight two-chain urokinase-plasminogen activator

<220>

<221> PEPTIDE

<222> (381) ... (386)

<223> Hexahistidin affinity tag

<400> 25

Met	Ala	Glu	Ser	His	Leu	Leu	Gln	Trp	Leu	Leu	Leu	Leu	Leu	Pro	Thr	
1				5				10						15		
Leu	Cys	Gly	Pro	Gly	Thr	Ala	Ala	Trp	Phe	Pro	Ile	Pro	Leu	Pro	Tyr	
			20					25					30			
Cys	Trp	Leu	Cys	Arg	Ala	Leu	Ile	Lys	Arg	Ile	Gln	Ala	Met	Ile	Pro	
		35					40					45				
Lys	Gly	Ala	Leu	Ala	Val	Ala	Val	Ala	Gln	Val	Cys	Arg	Val	Val	Pro	
	50					55					60					
Leu	Val	Ala	Gly	Gly	Ile	Cys	Gln	Cys	Leu	Ala	Glu	Arg	Tyr	Ser	Val	
65					70					75					80	
Ile	Leu	Leu	Asp	Thr	Leu	Leu	Gly	Arg	Met	Leu	Pro	Gln	Leu	Val	Cys	
				85					90					95		
Arg	Leu	Val	Leu	Arg	Cys	Ser	Met	Lys	Pro	Ser	Ser	Pro	Pro	Glu	Glu	
			100					105						110		
Leu	Lys	Phe	Gln	Cys	Gly	Gln	Lys	Thr	Leu	Arg	Pro	Arg	Phe	Lys	Ile	
		115					120					125				
Ile	Gly	Gly	Glu	Phe	Thr	Thr	Ile	Glu	Asn	Gln	Pro	Trp	Phe	Ala	Ala	
	130					135					140					
Ile	Tyr	Arg	Arg	His	Arg	Gly	Gly	Ser	Val	Thr	Tyr	Val	Cys	Gly	Gly	
145					150					155					160	
Ser	Leu	Ile	Ser	Pro	Cys	Trp	Val	Ile	Ser	Ala	Thr	His	Cys	Phe	Ile	
				165					170					175		
Asp	Tyr	Pro	Lys	Lys	Glu	Asp	Tyr	Ile	Val	Tyr	Leu	Gly	Arg	Ser	Arg	
			180					185					190			
Leu	Asn	Ser	Asn	Thr	Gln	Gly	Glu	Met	Lys	Phe	Glu	Val	Glu	Asn	Leu	
		195					200					205				
Ile	Leu	His	Lys	Asp	Tyr	Ser	Ala	Asp	Thr	Leu	Ala	His	His	Asn	Asp	
	210					215					220					
Ile	Ala	Leu	Leu	Lys	Ile	Arg	Ser	Lys	Glu	Gly	Arg	Cys	Ala	Gln	Pro	
225					230					235					240	
Ser	Arg	Thr	Ile	Gln	Thr	Ile	Cys	Leu	Pro	Ser	Met	Tyr	Asn	Asp	Pro	
				245					250					255		

Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser  
                   260                                  265                                  270  
 Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu  
                   275                                  280                                  285  
 Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val  
                   290                                  295                                  300  
 Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser  
 305                                  310                                  315                                  320  
 Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg  
                                   325                                  330                                  335  
 Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys  
                                   340                                  345                                  350  
 Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile  
                   355                                  360                                  365  
 Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu His His His His  
                   370                                  375                                  380  
 His His  
 385

<210> 26  
 <211> 383  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <221> SIGNAL  
 <222> (1) ... (20)  
 <223> Signal sequence of the human urokinase plasminogen activator

<220>  
 <221> PEPTIDE  
 <222> (21) ... (22)  
 <223> Linker

<220>  
 <221> PEPTIDE  
 <222> (23) ... (298)  
 <223> Human low molecular weight two-chain urokinase-plasminogen activator

<220>  
 <221> PEPTIDE  
 <222> (299) ... (377)  
 <223> Coding sequence of the mature human surfactant protein B

<220>  
 <221> PEPTIDE

<222> (378) ... (383)

<223> Hexahistidin affinity tag

<400> 26

Met	Arg	Ala	Leu	Leu	Ala	Arg	Leu	Leu	Leu	Cys	Val	Leu	Val	Val	Ser	
1				5					10					15		
Asp	Ser	Lys	Gly	Ser	Asn	Lys	Pro	Ser	Ser	Pro	Pro	Glu	Glu	Leu	Lys	
			20					25					30			
Phe	Gln	Cys	Gly	Gln	Lys	Thr	Leu	Arg	Pro	Arg	Phe	Lys	Ile	Ile	Gly	
		35					40					45				
Gly	Glu	Phe	Thr	Thr	Ile	Glu	Asn	Gln	Pro	Trp	Phe	Ala	Ala	Ile	Tyr	
	50					55					60					
Arg	Arg	His	Arg	Gly	Gly	Ser	Val	Thr	Tyr	Val	Cys	Gly	Gly	Ser	Leu	
65					70					75					80	
Ile	Ser	Pro	Cys	Trp	Val	Ile	Ser	Ala	Thr	His	Cys	Phe	Ile	Asp	Tyr	
			85						90					95		
Pro	Lys	Lys	Glu	Asp	Tyr	Ile	Val	Tyr	Leu	Gly	Arg	Ser	Arg	Leu	Asn	
			100					105					110			
Ser	Asn	Thr	Gln	Gly	Glu	Met	Lys	Phe	Glu	Val	Glu	Asn	Leu	Ile	Leu	
		115					120					125				
His	Lys	Asp	Tyr	Ser	Ala	Asp	Thr	Leu	Ala	His	His	Asn	Asp	Ile	Ala	
	130					135						140				
Leu	Leu	Lys	Ile	Arg	Ser	Lys	Glu	Gly	Arg	Cys	Ala	Gln	Pro	Ser	Arg	
145					150					155					160	
Thr	Ile	Gln	Thr	Ile	Cys	Leu	Pro	Ser	Met	Tyr	Asn	Asp	Pro	Gln	Phe	
			165						170					175		
Gly	Thr	Ser	Cys	Glu	Ile	Thr	Gly	Phe	Gly	Lys	Glu	Asn	Ser	Thr	Asp	
			180					185					190			
Tyr	Leu	Tyr	Pro	Glu	Gln	Leu	Lys	Met	Thr	Val	Val	Lys	Leu	Ile	Ser	
		195					200					205				
His	Arg	Glu	Cys	Gln	Gln	Pro	His	Tyr	Tyr	Gly	Ser	Glu	Val	Thr	Thr	
	210					215					220					
Lys	Met	Leu	Cys	Ala	Ala	Asp	Pro	Gln	Trp	Lys	Thr	Asp	Ser	Cys	Gln	
225					230					235					240	
Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Ser	Leu	Gln	Gly	Arg	Met	Thr	
			245					250						255		
Leu	Thr	Gly	Ile	Val	Ser	Trp	Gly	Arg	Gly	Cys	Ala	Leu	Lys	Asp	Lys	
		260					265						270			
Pro	Gly	Val	Tyr	Thr	Arg	Val	Ser	His	Phe	Leu	Pro	Trp	Ile	Arg	Ser	

275		280		285
His Thr Lys Glu Gln Asn Gly Leu Ala Leu Phe Pro Ile Pro Leu Pro				
290		295		300
Tyr Cys Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile				
305		310		315
Pro Lys Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val				
		325		330
Pro Leu Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser				
		340		345
Val Ile Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val				
		355		360
Cys Arg Leu Val Leu Arg Cys Ser Met His His His His His His				
370		375		380